



RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 10/629,329
Source: OIP
Date Processed by STIC: 8-18-03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
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OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/629,329

DATE: 08/18/2003

TIME: 09:10:27

Input Set : E:\Utsc761.app

Output Set: N:\CRF4\08182003\J629329.raw

3 <110> APPLICANT: DARNAY, BRYANT G.
 5 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS USING POLYNUCLEOTIDES AND
 6 POLYPEPTIDES OF RANK-ASSOCIATED INHIBITOR (RAIN)
 8 <130> FILE REFERENCE: UTSC:761US
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/629,329
 11 <141> CURRENT FILING DATE: 2003-07-29
 13 <150> PRIOR APPLICATION NUMBER: 60/399,205
 14 <151> PRIOR FILING DATE: 2002-07-29
 16 <160> NUMBER OF SEQ ID NOS: 23
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 729
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (1)..(729)
 29 <400> SEQUENCE: 1
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 32 1 5 10 15
 34 ggc gcg cag gac aag gag cat cca aga tac ctg atc cca gaa ctt tgc 96
 35 Gly Ala Gln Asp Lys Glu His Pro Arg Tyr Leu Ile Pro Glu Leu Cys
 36 20 25 30
 38 aaa cag ttt tac cat tta ggc tgg gtc act ggg act gga gga gga att 144
 39 Lys Gln Phe Tyr His Leu Gly Trp Val Thr Gly Thr Gly Gly Gly Ile
 40 35 40 45
 42 agc ttg aag cat ggc gat gaa atc tac att gct cct tca gga gtg caa 192
 43 Ser Leu Lys His Gly Asp Glu Ile Tyr Ile Ala Pro Ser Gly Val Gln
 44 50 55 60
 46 aag gaa cga att cag cct gaa gac atg ttt gtt tgt gat ata aat gaa 240
 47 Lys Glu Arg Ile Gln Pro Glu Asp Met Phe Val Cys Asp Ile Asn Glu
 48 65 70 75 80
 50 aag gac ata agt gga cct tcg cca tcg aag aag cta aaa aaa agc cag 288
 51 Lys Asp Ile Ser Gly Pro Ser Pro Ser Lys Lys Leu Lys Lys Ser Gln
 52 85 90 95
 54 tgt act cct ctt ttc atg aat gct tac aca atg aga gga gca ggt gca 336
 55 Cys Thr Pro Leu Phe Met Asn Ala Tyr Thr Met Arg Gly Ala Gly Ala
 56 100 105 110
 58 gtg att cat acc cac tct aaa gct gct gtg atg gcc aca ctt ctc ttt 384
 59 Val Ile His Thr His Ser Lys Ala Ala Val Met Ala Thr Leu Leu Phe
 60 115 120 125
 62 cca gga cgg gag ttt aaa att aca cat caa gag atg ata aaa gga ata 432

**Does Not Comply
Corrected Diskette Needed**

pp. 5-6

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Input Set : E:\Utsc761.app

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64      130                      135                      140
66 aag aaa tgt act tcc gga ggg tat tat aga tat gat gat atg tta gtg   480
67 Lys Lys Cys Thr Ser Gly Gly Tyr Tyr Arg Tyr Asp Asp Met Leu Val
68 145                      150                      155                      160
70 gta ccc att att gag aat aca cct gag gag aaa ggc ctc aaa gat aga   528
71 Val Pro Ile Ile Glu Asn Thr Pro Glu Glu Lys Gly Leu Lys Asp Arg
72                      165                      170                      175
74 atg gct cat gca atg aat gaa tac cca gac tcc tgt gca gta ctg gtc   576
75 Met Ala His Ala Met Asn Glu Tyr Pro Asp Ser Cys Ala Val Leu Val
76                      180                      185                      190
78 aga cgt cat gga gta tat gtg tgg ggg gaa aca tgg gag aag gcc aaa   624
79 Arg Arg His Gly Val Tyr Val Trp Gly Glu Thr Trp Glu Lys Ala Lys
80                      195                      200                      205
82 acc atg tgt gag tgt tat gac tat tta ttt gat att gcc gta tca atg   672
83 Thr Met Cys Glu Cys Tyr Asp Tyr Leu Phe Asp Ile Ala Val Ser Met
84      210                      215                      220
86 aag aaa gta gga ctt gat cct tca cag ctc cca gtt gga gaa aat gga   720
87 Lys Lys Val Gly Leu Asp Pro Ser Gln Leu Pro Val Gly Glu Asn Gly
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91 Ile Val
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95 <211> LENGTH: 242
96 <212> TYPE: PRT
97 <213> ORGANISM: Homo sapiens
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103                      20                      25                      30
104 Lys Gln Phe Tyr His Leu Gly Trp Val Thr Gly Thr Gly Gly Gly Ile
105                      35                      40                      45
106 Ser Leu Lys His Gly Asp Glu Ile Tyr Ile Ala Pro Ser Gly Val Gln
107 50                      55                      60
108 Lys Glu Arg Ile Gln Pro Glu Asp Met Phe Val Cys Asp Ile Asn Glu
109 65                      70                      75                      80
110 Lys Asp Ile Ser Gly Pro Ser Pro Ser Lys Lys Leu Lys Lys Ser Gln
111                      85                      90                      95
112 Cys Thr Pro Leu Phe Met Asn Ala Tyr Thr Met Arg Gly Ala Gly Ala
113                      100                      105                      110
114 Val Ile His Thr His Ser Lys Ala Ala Val Met Ala Thr Leu Leu Phe
115                      115                      120                      125
116 Pro Gly Arg Glu Phe Lys Ile Thr His Gln Glu Met Ile Lys Gly Ile
117      130                      135                      140
118 Lys Lys Cys Thr Ser Gly Gly Tyr Tyr Arg Tyr Asp Asp Met Leu Val
119 145                      150                      155                      160
120 Val Pro Ile Ile Glu Asn Thr Pro Glu Glu Lys Gly Leu Lys Asp Arg
121                      165                      170                      175

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Input Set : E:\Utsc761.app

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123      180      185      190
124 Arg Arg His Gly Val Tyr Val Trp Gly Glu Thr Trp Glu Lys Ala Lys
125      195      200      205
126 Thr Met Cys Glu Cys Tyr Asp Tyr Leu Phe Asp Ile Ala Val Ser Met
127      210      215      220
128 Lys Lys Val Gly Leu Asp Pro Ser Gln Leu Pro Val Gly Glu Asn Gly
129 225      230      235      240
130 Ile Val
134 <210> SEQ ID NO: 3
135 <211> LENGTH: 726
136 <212> TYPE: DNA
137 <213> ORGANISM: Mus musculus
139 <220> FEATURE:
140 <221> NAME/KEY: CDS
141 <222> LOCATION: (1)..(726)
143 <400> SEQUENCE: 3
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146 1      5      10      15
148 gcg cag gac aag gag cac ccc cga ttc ctg atc cca gaa ctt tgc aaa 96
149 Ala Gln Asp Lys Glu His Pro Arg Phe Leu Ile Pro Glu Leu Cys Lys
150      20      25      30
152 cag ttt tac cat ctg ggc tgg gtc acc ggc act gga ggg gga atc agc 144
153 Gln Phe Tyr His Leu Gly Trp Val Thr Gly Thr Gly Gly Ile Ser
154      35      40      45
156 ttg aag cat ggc aat gaa atc tac att gct ccc tca ggc gtg caa aag 192
157 Leu Lys His Gly Asn Glu Ile Tyr Ile Ala Pro Ser Gly Val Gln Lys
158      50      55      60
160 gaa cgc att cag cca gaa gac atg ttt gtg tgt gac att aat gag cag 240
161 Glu Arg Ile Gln Pro Glu Asp Met Phe Val Cys Asp Ile Asn Glu Gln
162 65      70      75      80
164 gac ata agc ggg cct cca gca tct aag aag ctg aaa aaa agc cag tgc 288
165 Asp Ile Ser Gly Pro Pro Ala Ser Lys Lys Leu Lys Lys Ser Gln Cys
166      85      90      95
168 act cct ctt ttc atg aat gct tat acc atg aga gga gct ggc gca gtg 336
169 Thr Pro Leu Phe Met Asn Ala Tyr Thr Met Arg Gly Ala Gly Ala Val
170      100      105      110
172 att cat acc cac tct aaa gct gct gtg atg gct acc ctt ctg ttt cca 384
173 Ile His Thr His Ser Lys Ala Ala Val Met Ala Thr Leu Leu Phe Pro
174      115      120      125
176 gga cag gag ttt aaa att aca cat caa gag atg atc aaa gga ata agg 432
177 Gly Gln Glu Phe Lys Ile Thr His Gln Glu Met Ile Lys Gly Ile Arg
178      130      135      140
180 aaa tgt acc tca gga ggc tat tac aga tac gat gat atg tta gtg gta 480
181 Lys Cys Thr Ser Gly Gly Tyr Tyr Arg Tyr Asp Asp Met Leu Val Val
182 145      150      155      160
184 cct att att gag aac act cct gaa gag aag gat ctc aaa gaa agg atg 528
185 Pro Ile Ile Glu Asn Thr Pro Glu Glu Lys Asp Leu Lys Glu Arg Met

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Input Set : E:\Utsc761.app

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186          165          170          175
188 gct cat gcc atg aac gag tac cca gac tcc tgt gcg gtt ctt gtc cgg 576
189 Ala His Ala Met Asn Glu Tyr Pro Asp Ser Cys Ala Val Leu Val Arg
190          180          185          190
192 cgt cat ggg gtg tac gtg tgg gga gaa aca tgg gag aaa gca aaa acc 624
193 Arg His Gly Val Tyr Val Trp Gly Glu Thr Trp Glu Lys Ala Lys Thr
194          195          200          205
196 atg tgt gag tgt tat gac tac ctg ttt gac att gct gtc tcc atg aag 672
197 Met Cys Glu Cys Tyr Asp Tyr Leu Phe Asp Ile Ala Val Ser Met Lys
198          210          215          220
200 aag atg gga ctc gat cca aca cag ctc cca gtt gga gaa aat gga att 720
201 Lys Met Gly Leu Asp Pro Thr Gln Leu Pro Val Gly Glu Asn Gly Ile
202 225          230          235          240
204 gtg taa 726
205 Val
208 <210> SEQ ID NO: 4
209 <211> LENGTH: 241
210 <212> TYPE: PRT
211 <213> ORGANISM: Mus musculus
213 <400> SEQUENCE: 4
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215 1 5 10 15
216 Ala Gln Asp Lys Glu His Pro Arg Phe Leu Ile Pro Glu Leu Cys Lys
217 20 25 30
218 Gln Phe Tyr His Leu Gly Trp Val Thr Gly Thr Gly Gly Ile Ser
219 35 40 45
220 Leu Lys His Gly Asn Glu Ile Tyr Ile Ala Pro Ser Gly Val Gln Lys
221 50 55 60
222 Glu Arg Ile Gln Pro Glu Asp Met Phe Val Cys Asp Ile Asn Glu Gln
223 65 70 75 80
224 Asp Ile Ser Gly Pro Pro Ala Ser Lys Lys Leu Lys Lys Ser Gln Cys
225 85 90 95
226 Thr Pro Leu Phe Met Asn Ala Tyr Thr Met Arg Gly Ala Gly Ala Val
227 100 105 110
228 Ile His Thr His Ser Lys Ala Ala Val Met Ala Thr Leu Leu Phe Pro
229 115 120 125
230 Gly Gln Glu Phe Lys Ile Thr His Gln Glu Met Ile Lys Gly Ile Arg
231 130 135 140
232 Lys Cys Thr Ser Gly Gly Tyr Tyr Arg Tyr Asp Asp Met Leu Val Val
233 145 150 155 160
234 Pro Ile Ile Glu Asn Thr Pro Glu Glu Lys Asp Leu Lys Glu Arg Met
235 165 170 175
236 Ala His Ala Met Asn Glu Tyr Pro Asp Ser Cys Ala Val Leu Val Arg
237 180 185 190
238 Arg His Gly Val Tyr Val Trp Gly Glu Thr Trp Glu Lys Ala Lys Thr
239 195 200 205
240 Met Cys Glu Cys Tyr Asp Tyr Leu Phe Asp Ile Ala Val Ser Met Lys
241 210 215 220
242 Lys Met Gly Leu Asp Pro Thr Gln Leu Pro Val Gly Glu Asn Gly Ile

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Input Set : E:\Utsc761.app

Output Set: N:\CRF4\08182003\J629329.raw

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243 225                230                235                240
244 Val
248 <210> SEQ ID NO: 5
249 <211> LENGTH: 34
250 <212> TYPE: PRT
251 <213> ORGANISM: Artificial Sequence
W--> 253 <220> FEATURE:
W--> 253 <223> OTHER INFORMATION: See page 6
W--> 253 <400> 5
254 Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Ala Pro
255   1                5                10                15
257 Lys Thr Leu Lys Asp Arg Met Ala His Ala Met Asn Glu Tyr Pro Asp
258                20                25                30
260 Ser Cys
264 <210> SEQ ID NO: 6
265 <211> LENGTH: 34
266 <212> TYPE: PRT
267 <213> ORGANISM: Artificial Sequence
269 <220> FEATURE:
270 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
271     Peptide
273 <400> SEQUENCE: 6
274 Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Ala Pro
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277 Lys Thr Leu Ala Asp Ala Met Ala His Thr Met Asn Glu Tyr Pro Asp
278                20                25                30
280 Ser Cys
284 <210> SEQ ID NO: 7
285 <211> LENGTH: 30
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
291     Primer
293 <400> SEQUENCE: 7
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298 <211> LENGTH: 33
299 <212> TYPE: DNA
300 <213> ORGANISM: Artificial Sequence
302 <220> FEATURE:
303 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
304     Primer
306 <400> SEQUENCE: 8
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310 <210> SEQ ID NO: 9
311 <211> LENGTH: 33
312 <212> TYPE: DNA
313 <213> ORGANISM: Artificial Sequence

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RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 08/18/2003

PATENT APPLICATION: US/10/629,329

TIME: 09:10:28

Input Set : E:\Utsc761.app

Output Set: N:\CRF4\08182003\J629329.raw

Use of <220> Feature(NEW RULES):

Sequence(s) __ are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec. 1.823 of new Rules)

Seq#:5

VERIFICATION SUMMARYPATENT APPLICATION: **US/10/629,329**

DATE: 08/18/2003

TIME: 09:10:28

Input Set : **E:\Utsc761.app**Output Set: **N:\CRF4\08182003\J629329.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:253 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:253 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:253 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:253